

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 09:23:09 ; Search time 11.3094 Seconds

(without alignments)
2442.495 Million cell updates/sec

Title: US-09-836-077-3

Perfect score: 3615

Sequence: 1 MTPEPPGRAPRSAPRRVPG.....LAASLWGLVPLTFLGLLVH 666

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Archived: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3615	100.0	666	SM7A_HUMAN	075326 homo sapien
2	3214	88.9	664	SM7A_MOUSE	09498 mus musculu
3	654.5	18.1	771	SM3A_HUMAN	014563 homo sapien
4	635	17.6	772	SM3A_MOUSE	008665 mus musculu
5	632.5	17.5	772	SM3A_CHICK	090607 gallus gall
6	628.5	17.4	748	SM3B_MOUSE	062177 mus musculu
7	623	17.2	772	SM3A_RAT	063548 rattus norv
8	621	17.2	860	SZ1A_BRARE	09w7j1 brachydanio
9	617	17.1	749	SM3B_HUMAN	013214 homo sapien
10	617	17.1	782	SM4B_MOUSE	062179 mus musculu
11	613	17.0	778	SZ1B_BRARE	09w686 brachydanio
12	598.5	16.6	861	SM4D_MOUSE	009126 mus musculu
13	597.5	16.5	751	SM3C_MOUSE	062181 mus musculu
14	597	16.5	785	SM3F_MOUSE	013575 homo sapien
15	595.5	16.5	764	SM22_BRARE	09w696 brachydanio
16	591.5	16.4	751	SM3C_HUMAN	099885 homo sapien
17	588.5	16.3	673	SM4B_HUMAN	099822 homo sapien
18	582	16.1	785	SM3E_MOUSE	088632 mus musculu
19	575	15.9	751	SM3C_CHICK	042236 gallus gall
20	570	15.8	862	SM4D_HUMAN	092854 homo sapien
21	567.5	15.7	775	SM3E_HUMAN	015041 homo sapien
22	565	15.6	761	SM3D_CHICK	090663 gallus gall
23	555	15.4	775	SM3E_MOUSE	095075 mus musculu
24	548.5	15.2	777	SM3D_HUMAN	095025 homo sapien
25	538.5	14.9	785	SM2E_CHICK	042237 gallus gall
26	536	14.8	770	SM4F_HUMAN	094754 homo sapien
27	525.5	14.5	766	SM7X_BRARE	09ytx4 brachydanio
28	515.5	14.3	777	SM4F_MOUSE	092123 mus musculu
29	510	14.1	776	SM4F_RAT	092143 rattus norv
30	506.5	14.0	838	SM4G_HUMAN	094919 homo sapien
31	491.5	13.6	837	SM4G_MOUSE	094917 mus musculu
32	485.5	13.4	760	SM4A_MOUSE	062178 mus musculu
33	482.5	13.3	762	SM4A_HUMAN	09h351 homo sapien

34	479.5	13.3	834	1	SM4C_MOUSE	064151 mus musculu
35	452	12.5	730	1	SM1A_SCHAM	026473 schistocerc
36	435	12.0	295	1	SM4D_CHICK	090665 gallus gall
37	419	11.6	697	1	SM2A_SCHGR	09x2c8 schistocerc
38	418	11.6	888	1	SM6A_MOUSE	035464 mus musculu
39	411	11.4	712	1	SM1A_CAEL	017330 caenorhabd1
40	409	11.3	1074	1	SM5A_HUMAN	013591 homo sapien
41	408	11.3	712	1	SM1A_HUMAN	026972 tribolium c
42	407	11.3	771	1	SM1A_TRICF	024322 drosophila
43	407	11.3	1093	1	SM5B_MOUSE	060519 mus musculu
44	403	11.1	1077	1	SM5A_MOUSE	062217 mus musculu
45	402	11.1	706	1	SM2A_DROME	024323 drosophila

ALIGNMENTS

RESULT 1	ID	SM7A_HUMAN	STANDARD:	PRT:	666 AA.
AC	075326:				
DT	16-OCT-2001 (rel. 40, Created)				
DT	16-OCT-2001 (rel. 40, Last sequence update)				
DT	16-OCT-2001 (rel. 40, Last annotation update)				
DE	Semaphorin 7A precursor (Semaphorin L) (Sema L) (Semaphorin				
DE	K1) (Sema K1) (John-Milton-Hargen Blood group Ag) (JMH blood				
DE	group antigen) (CD108 antigen) (CDw108).				
GN	SEMA7A OR SEMAL OR CD108.				
OC	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98389619; PubMed=9721204;				
RA	Lange C., Liehr T., Goen M., Gebhart E., Fleckenstein B., Ensser A.;				
RT	"New eukaryotic semaphorins with close homology to semaphorins of DNA				
RT	viruses.";				
RL	Genomics 51:340-350(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99218431; PubMed=10201933;				
RA	Yamada A., Kubo K., Takeshita T., Harashima N., Kawano K., Mine T.,				
RA	Sagawa K., Sugamura K., Itoh K.;				
RT	"Molecular cloning of a glycosylphosphatidylinositol-anchored molecule				
RT	CDw108.";				
RL	J. Immunol. 162:4094-4100(1999).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RT	TISSUE=Placenta;				
RX	MEDLINE=98380463; PubMed=9712866;				
RA	Xu X., Ng S., Wu Z.-L., Nguyen D., Homburger S., Seidel-Dugan C.,				
RA	Ebens A., Luo Y.;				
RT	"Human semaphorin K1 is glycosylphosphatidylinositol-linked and				
RT	defines a new subfamily of viral-related semaphorins.";				
RL	J. Biol. Chem. 273:22428-22434(1998).				
RN	[4]				
RP	CHARACTERIZATION.				
RX	MEDLINE=99344620; PubMed=10416131;				
RA	Angelisova P., Drbal K., Cerny J., Hlilert I., Horejsi V.;				
RT	"Characterization of the human leukocyte GPI-anchored glycoprotein				
RT	CDw108 and its relation to other similar molecules.";				
RL	Immunobiology 200:234-245(1999).				
CC	- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE NERVOUS SYSTEM AND IN				
CC	MODULATING IMMUNE FUNCTION.				
CC	- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.				
CC	- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, TESTIS, OVARY, SPLEEN,				
CC	BRAIN, SPINAL CHORD, LUNG, HEART, ADRENAL GLAND, LYMPH NODES,				
CC	THYMUS, INTESTINE AND KIDNEY.				
CC	- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.				
CC	- SIMILARITY: CONTAINS 1 SEMA DOMAIN.				
CC	- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.				

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CC EMBL; AF030698; AAC34261.1; -
 CC EMBL; AF030697; AAC34741.1; -
 CC EMBL; AF069493; AAC82642.1; -
 CC EMBL; AF071542; AAC80456.1; -
 CC Gene: HGNC:10741; SEMA7A.
 CC InterPro: IPR003599; Ig.
 CC InterPro: IPR003659; Plexin-like.
 CC InterPro: IPR01627; Sema.
 CC Pfam: PF01403; Sema; 1.
 CC SMART: SM00409; IG; 1.
 CC SMART: SM00423; PSI; 1.
 CC Signal: Immunoglobulin domain; Multigene family; Neurogenesis;
 CC Developmental protein; Glycoprotein; GPI-anchor.
 CC SIGNAL 1 44
 CC CHAIN 45 648
 CC PROPEP 649 666
 CC DOMAIN 75 474
 CC SITE 267 620
 CC SITE 648 648
 CC LIPID 566 613
 CC DISULFID 105 105
 CC CARBOHYD 157 157
 CC CARBOHYD 258 258
 CC CARBOHYD 330 330
 CC CARBOHYD 602 602
 CC SEQUENCE 666 AA; 74823 MW; AD3AB56B5EBE194 CRC64;
 Query Match 100.0%; Score 3615; DB 1; Length 666;
 Best Local Similarity 100.0%; Pred. No. 1.9e-265;
 Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPPPGPAAPSAAPARAVGPAPRLGLRLRLLLMAAASAOCHLRSGPRFAVMKG 60
 DB 1 MTPPPGPAAPSAAPARAVGPAPRLGLRLRLLLMAAASAOCHLRSGPRFAVMKG 60
 QY 61 HVGQDRVDFGQTEPHTVLFHEPGSSVWVGGRKGYLDFEPGKNAVTVNIGSTKGC 120
 DB 61 HVGQDRVDFGQTEPHTVLFHEPGSSVWVGGRKGYLDFEPGKNAVTVNIGSTKGC 120
 QY 121 LDKRCENVITLLERRSEGLACGTNARHPSCMNLVNGTVPLGEMRGYAPSPDENSIV 180
 DB 121 LDKRCENVITLLERRSEGLACGTNARHPSCMNLVNGTVPLGEMRGYAPSPDENSIV 180
 QY 181 LFEQDEVYSTRKQYNGKIPFRFRIRGESELYTSDTYWQNPQFIKATTVHDOAVDDKI 240
 DB 181 LFEQDEVYSTRKQYNGKIPFRFRIRGESELYTSDTYWQNPQFIKATTVHDOAVDDKI 240
 QY 241 YFFPEDNDPKKPEAPLNVSRVAOLCRGQGGESSLSKMTFLKAMVYCDATANKNF 300
 DB 241 YFFPEDNDPKKPEAPLNVSRVAOLCRGQGGESSLSKMTFLKAMVYCDATANKNF 300
 QY 301 NRIQDVFLLPSPSGQWRDTRVYGVSNPMNYSAVCVYSLGDDIKKFRISLKGHYSSLPN 360
 DB 301 NRIQDVFLLPSPSGQWRDTRVYGVSNPMNYSAVCVYSLGDDIKKFRISLKGHYSSLPN 360
 QY 361 PRPGKCLPDQPIPTETFOVADRHEVAQVRPEMPLKTPLEHSKYHYOKVAHMQASH 420
 DB 361 PRPGKCLPDQPIPTETFOVADRHEVAQVRPEMPLKTPLEHSKYHYOKVAHMQASH 420
 QY 421 GETFHVLTLDKRGTIHKVNEVEGEHSAFARINMEIQPFRRAAAIQIMSLEAKKLYVS 480
 DB 421 GETFHVLTLDKRGTIHKVNEVEGEHSAFARINMEIQPFRRAAAIQIMSLEAKKLYVS 480
 QY 481 SOMEVSQVPLDCEVYGGGCHGLMSRDPYCGWMDGRCISYSSRSVLSINPAEPHKE 540

DB 481 SOMEVSQVPLDCEVYGGGCHGLMSRDPYCGWMDGRCISYSSRSVLSINPAEPHKE 540
 QY 541 CPMPKDKAPLOKVSILAPNSRYLSCPMESRHAITYSMRKHENEQSCFPHOSPNILRT 600
 DB 541 CPMPKDKAPLOKVSILAPNSRYLSCPMESRHAITYSMRKHENEQSCFPHOSPNILRT 600
 QY 601 ENLTAQOYGHYFCEAOEGSYFREAOHQMLLPEDGINAEHLGHACALASLWGLVPLTL 660
 DB 601 ENLTAQOYGHYFCEAOEGSYFREAOHQMLLPEDGINAEHLGHACALASLWGLVPLTL 660
 QY 661 LGGLVH 666
 DB 661 LGGLVH 666

RESULT 2
 SM7A_MOUSE
 ID SM7A_MOUSE STANDARD; PRT; 664 AA.
 AC 09QUR8; 086371;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Semaphorin 7A precursor (Semaphorin L) (Sema L) (Semaphorin K1) (Sema K1) (CD108 antigen) (CDW108).
 GN SEMA7A OR SEMK1 OR SEMAL OR CD108.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99096477; PubMed=9878861;
 RA Sato Y., Takahashi H.;
 RT "Molecular cloning and expression of murine homologue of semaphorin K1 gene."
 RL Biochim. Biophys. Acta 1443:419-422(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=98389619; PubMed=9721204;
 RA Lange C., Liehr T., Goen M., Gebhart E., Fleckenstein B., Essner A.;
 RT "New eukaryotic semaphorins with close homology to semaphorins of DNA viruses."
 RL Genomics 51:340-350(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=20340072; PubMed=10885563;
 RA Mine T., Harada K., Matsumoto T., Yamana H., Shirouzu K., Itoh K., Yamada A.;
 RT "Cw108 expression during T-cell development."
 RL Tissue Antigens 55:429-436(2000).
 CC - FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE NERVOUS SYSTEM AND IN MODULATING IMMUNE FUNCTION.
 CC - SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC - TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN. LOWER IN HEART, THYMUS, SPLEEN, TESTIS AND OVARY. THE EXPRESSION INCREASES IN LATE EMBRYONIC AND POSTNATAL STAGES.
 CC - SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
 CC - SIMILARITY: CONTAINS 1 SEMA DOMAIN.
 CC - SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
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Query Match 18.1%; Score 654.5; DB 1; Length 771;
 Best Local Similarity 28.2%; Pred. No. 1,10e-41;
 Matches 194; Conservative 115; Mismatches 280; Indels 99; Gaps 27.

FT	DOMAIN	642	729	IG-LIKE C2-TYPE DOMAIN.
FT	DISULFID	649	722	ARG/LYS-RICH (BASIC).
FT	CARBOHYD	53	53	BY SIMILARITY
FT	CARBOHYD	125	125	N-LINKED (GLICNAC. . .) (POTENTIAL).
FT	CARBOHYD	590	590	N-LINKED (GLICNAC. . .) (POTENTIAL).
FT	SEQUENCE	771 AA:	88889 MM;	9985F8D33EAE8456 CRC64;
SO				
OY	32	RLLLLLMAAASAGHLNSG----	PRFAVMKGHVGDHYD----	FGOTEPHYLFHEP 82
DB	6	RIVCFMGVLLTARANYONGKNNVPRLKSYKEMLESNVITFNGLIANSSTYTFLEDEE 65		
OY	83	GSSSVWVGGRGVVYLFDPREGKNASRVYVNIISTK-----	GSCLDKRDCENYITLLER 135	
DB	66	RSRLVYGKDHIDFSDLVNINDFOKIYWPVSYTRDECKMAGKDLTK-ECANFIKVLVA 123		
OY	136	RSE-GLLACGTARAPRSPCWNLVNGTVVPLGEM-----	RGVAPFSDENS 178	
DB	124	YNQTHLYACGTGAPRPIG-----IYELIDGHPEDNIIFKLNSHFENGSGKRPDYDKLLT 177		
OY	179	LVLEFGDEVYSTRKQEVYKGIPTRRRIIGSEELTY---SDTVMONPQITKATYHQ-DQ 234		
DB	178	ASLLIDGELYSYGTADAFMGRDFAIRFTGLHNHPIRTEODHSRWLMDPKFISAHILISEDN 237		
OY	235	AYDDKIYFFERDNDPKNEAPLANSRVVQLCRGDGSGSSLSVSKWNTFLKAMLYCSDA 294		
DB	238	PEDDKIVYFFERNALIDGHSKATARIQIOICKNDFGGHRL-VKNWITFLKARLLICSPV 296		
OY	295	ATN---KMFNRLQDYVLL--PDPSQMDRTRYGVF---SNFWNTSAVCVYSLGDIDKVF 346		
DB	297	GPNGIDTFHDELDQYDFLNMFKDP---KNPVYGVYFTSSNTEFKGSAYCVMYSMDVRVF 352		
OY	347	-----RTSSLKGYSLLPNPRPGK-----LPDQDIPETPEGVADRNHEVAQR 390		
DB	353	LGPYAHROGPNQWVPYQGRVYPRPRGTCSPKSTFGGFSDBTKLPDDVITFAASHPAMNYP 412		
OY	391	VEPMG---PLKTPLEHSKYHYQKVAVHRMQASHETFEVLYLTDRGTIHKVE--PGHQ 445		
DB	413	VEPMNRPPIVITDY---NYQFTQIVVDVDAEDGQ-YDVMFIGTDVGTALVKVSIPIKET 468		
OY	446	EHSFANFM-ELQPRRAALIQTMSLDARRLKLYSSQMEVSOVPLDCEVGGGCGHCL 504		
DB	469	WDLDEVLLEETVTRPEPTAISAMELSTQDQYLGSTAGVACVADLPYHNRCDIYGGKCAECQ 528		
OY	505	MSRDEYCGMDGRCISIV--SSERSVLOSINAPBHKECGNPKPDK---APLQKYL-A 557		
DB	529	LARDPYCAMDGSAGCRYPPTAKRRTRRDIDRNGDPLTHSDLHNDHNNHSHSEERKIYGV 588		
OY	558	PNRSRYLSCPMESRHATYVSMRHKENEVQSCERGHOSPNCI-----LFTENLTADQYGYHF 612		
DB	589	ENSSFTFLCSPSQSALYVWQFORNEERKEEIRVDHIIITRDQGLLRSLQOKDSGNYL 648		
OY	613	CEAOGSYFREAOHQWLLPEDGIMAEHL 640		
DB	649	CHAVEHGFTQTLKLYTL---EVIDTEHL 673		
RESULT 4				
SM3A.MOUSE	STANDARD:	PRT:	772 AA.	
ID	SM3A.MOUSE			
AC	008665; 062180; 062215;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Semaphorin 3A precursor (Semaphorin III) (Sema III) (Semaphorin D) (Sema D).			
GN	SEM3A OR SEM4D OR SEMD.			
OC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

OC	Mammalia	Eutheria;	Rodentia;	Sciurognathi;	Muridae;	Murinae;	Mus.
OX	NCBI_TaxID=10090;						
RN	[1]	SEQUENCE FROM N.A.					
RC	STRAIN=NMRI;	TISSUE=Embryo;					
RX	MEDLINE=95267431;	PubMed=7748561;					
RA	Pueschel A.W., Adams R.H., Betz H.;						
RT	"Murine semaphorin D/collapsin is a member of a diverse gene family						
RL	and creates domains inhibitory for axonal extension.";						
RM	Neuron 14:941-948(1995).						
RN	[2]	SEQUENCE FROM N.A.					
RA	MEDLINE=97470885;	PubMed=9331345;					
RT	Taniguchi M., Yusa S., Fujisawa H., Naruse I., Saga S., Mishina M.,						
RL	Yagi T.;						
RM	"Disruption of semaphorin II/D gene causes severe abnormality in						
RN	peripheral nerve projection.";						
RM	Neuron 19:519-530(1997).						
RN	[3]	SEQUENCE FROM N.A.					
RA	Kimura T., Fishman M.C.;						
RT	"cDNA sequence of mouse collapsin/semaphorin III.";						
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.						
RN	[4]	SEQUENCE OF 107-772 FROM N.A.					
RC	TISSUE=Fetal brain;						
RX	MEDLINE=95267432;	PubMed=7748562;					
RA	Messersmith E.K., Leonardo E.D., Shatz C.J., Tessier-Lavigne M.,						
RT	Goodman C.S., Kolodkin A.L.;						
RL	"Semaphorin III can function as a selective chemorepellent to pattern						
RM	sensory projections in the spinal cord.";						
RM	Neuron 14:949-959(1995).						
CC	-I- FUNCTION: PLAY A ROLE IN GROWTH CONES GUIDANCE. MAY FUNCTION TO						
CC	PATTERN SENSORY PROJECTIONS BY SELECTIVELY REPELLING AXONS THAT						
CC	NORMALLY TERMINATE DORSALLY.						
CC	-I- SUBCELLULAR LOCATION: Secreted.						
CC	-I- DEVELOPMENTAL STAGE: EXPRESSED EARLY IN EMBRYONIC DEVELOPMENT						
CC	(E11) IN DISTINCT REGIONS OF THE NEUROECTODERM AND MESODERM.						
CC	EXPRESSION BECAME MORE EXTENSIVE AT LATER STAGES.						
CC	-I- DOMAIN: STRONG BINDING TO NEROPILIN IS MEDIATED BY THE CARBOXY						
CC	THIRD OF THE PROTEIN.						
CC	-I- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.						
CC	-I- SIMILARITY: CONTAINS 1 SEMA DOMAIN.						
CC	-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.						
CC	-----						
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration						
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).						
CC	-----						
DR	EMBL; X85993; CAAS9985.1; -						
DR	EMBL; D85028; BAA19773.1; -						
DR	EMBL; LA1541; AAL77611.1; -						
DR	EMBL; LA0848; AAA73934.1; -						
DR	MGI; MGI:107558; Sema3a.						
DR	InterPro; IPR003599; Ig.						
DR	InterPro; IPR003006; Ig_MHC.						
DR	InterPro; IPR003659; Plexin-like.						
DR	InterPro; IPR001627; Sema.						
DR	Pfam; PF00047; Ig; 1.						
DR	Pfam; PF01403; Sema; 1.						
DR	SMART; SM00409; Ig; 1.						
DR	SMART; SM00423; PSI; 1.						
KW	Signal, Immunoglobulin domain; Multigene family; Neurogenesis;						
KW	Developmental protein; Glycoprotein.						
FT	SIGNAL 1 20	POTENTIAL.					
FT	CHAIN 21 772	SEMAPHORIN 3A.					
FT	DOMAIN 240 538	SEMA.					
FT	DOMAIN 643 730	IG-LIKE C2-TYPE DOMAIN.					
FT	DOMAIN 728 770	ARG/LYS-RICH (BASIC)..					

FT DISULFID 650 723 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 193 193 D -> N (IN REF. 4).
 FT CONFLICT 207 207 H -> D (IN REF. 1).
 FT CONFLICT 253 253 D -> G (IN REF. 1).
 FT CONFLICT 352 352 F -> L (IN REF. 4).
 FT CONFLICT 403 403 A -> G (IN REF. 1).
 FT CONFLICT 571 572 OH -> ED (IN REF. 1).
 FT CONFLICT 616 620 EDRKE -> RSKR (IN REF. 1).
 FT CONFLICT 623 623 R -> K (IN REF. 4).
 SQ SEQUENCE 772 AA; 88799 MW; E89A08528B10AEC3 CRC64;

Query Match 17.6%; Score 635; DB 1; Length 772;
 Best Local Similarity 27.9%; Pred. No. 3.3e-40;
 Matches 192; Conservative 109; Mismatches 281; Indels 106; Gaps 27;

36 LMAAASAOGLRSG---PRIFAVMKGVGQDRVD-----FCQTEPHTVLFHEPGSS 86
 10 LFWGLTLARANYANGKNNVPRKLSTYKEMLESNNVITFNGLANSSVHTFLDDE-RSR 68
 87 VWVGGRKGYLLDFPEPGKNAVRYVNICSTK-----GSLDKKDCENYITLLERRSE- 138
 69 LYVGAKDHIFSFNLVNIKDFOKIWPVSVYTRDECKMAGKDIK-ECANFIKYLEAVNOT 127
 139 GLACGTARHPSCNNLVNGTVVPLGEM-----RGYAFSPDENSLVLF 182
 128 HLYAGCTGAFHPICT-----TYIEVGHHPEDNIEFKLQDSHFENGRKSKSYDRLKLASLL 181
 183 EGDEVYSTIRKQYNGKIPRRIRGESELYT---SDVWMPNPFKATIV-HODAYVD 238
 182 IDGELYSGADEFMRDAIFRTLGHHNPITREQDSRWLNDPRFISALHLESDNPED 241
 239 KIYTFREDNPKNAPLANSRVNQLCRGQGGSSLSVSKWNTFLKMLVCSDAATN- 297
 242 KYEFFFFENALDGEHSGKATARIQICNDKDFGHRSL-VNWTFTFLKRLKLSVGPNG 300
 298 --KNNRRLQDVFLL--PDPGQWRDTRVYGVF---SNPNYSAVCVYSLGDIKDYF---- 346
 301 IDTHDELQDVFLLMSKDP-----KNPIYGVTTSSNIFKGSAAVCMTSISDVRVFLGTY 356
 347 -----RTSSLKGYHSSLPRPRGKC-----LPDQDPIRTETFOVADRHPVAVQREPM 394
 357 AHRDGPVQWVYQGRVPRPRGTCPSKTFGGFDSFKDLRDPDVITFARSHPRAMVNPVFI 416
 395 G-----PLKTPLEHSKYHOKAVNHKMSHGETFENVLYTTTRGTTHKYYE--PGQESHF 449
 417 NNRPIMIKTDV---NYQFTQIVVDYDADGQ-YDVMFTGTVGVTLKVVSVPKETWHDL 472
 450 AFNIM-EIOPFRRAAIIQMSLDAERKLYVSSQWESVQVPLDLEVVGGGCHGLMSRD 508
 473 EYVLEEMTVFERPTTISAMELSTKQOOLYIGTAGVADLPRLHRCDIYKACAECCCLAD 532
 509 PYCGMDGRCISIV--SSERSVLOSTINPAERPKCCPN-----PKRDKAPLOKVSIA 557
 533 PYCADGSSCSYFPYAKRRTRRDIRNGDPLTHCSDLQHNHNHGRPSLEERITYGVE-- 590
 558 PMSRYYLQSPMSRHATYSMRKKEVQSCFEGHOSPNQI-----LFENLTAQOYGHNF 612
 591 -NSSTFLGCSPKSQRLVYVQFORNEDRKEEIRMGDHIITREGQILLRSLQKOSGNL 649
 613 CEAGSGYFREAOHWOLLPEGDIMAETHL 640
 650 CHAVEHGMQTLKYTL---EYIDTEHL 674

RESULT 5
 SM3A_CHICK STANDARD; PRT: 772 AA.
 AC 090607;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)
 DE Semaphorin 3A precursor (Collapsin-1) (COLL-1).
 GN SEM3A OR COLL.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 322-329; 362-372; 395-403 AND
 RP 666-680.
 RC TISSUE=Brain;
 RX MEDLINE=94006554; PubMed=8402908;
 RA Luo Y., Raible D., Raper J.A.;
 RT "Collapse of a protein in brain that induces the collapse and paralysis
 RT of neuronal growth cones";
 RL Cell 75:217-227(1993).
 CC -1- FUNCTION: INDUCES THE COLLAPSE AND PARALYSIS OF NEURONAL GROWTH
 CC CONES. COULD SERVE AS A LIGAND THAT GUIDES SPECIFIC GROWTH CONES
 CC BY A MOTILITY-INHIBITING MECHANISM. BINDS TO NEUROPILIN.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN BRAIN
 CC AND MUSCLE. MODERATE LEVELS IN LIVER, COLLAPASIN-1, -2, -3, AND -5 BIND TO
 CC OVERLAPPING BUT DISTINCT AXON TRACTS.
 CC -1- DOMAIN: STRONG BINDING TO NEUROPILIN IS MEDIATED BY THE CARBOXY
 CC THIRD OF THE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
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 CC
 DR EMBL: 002528; AAC59638.1; -
 DR InterPro: IPR003599; Ig_MHC.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003659; Plexin-like.
 DR InterPro: IPR001627; Sema.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF01403; Sema; 1.
 DR SMART: SM00409; Ig; 1.
 DR SMART: SM00423; PSI; 1.
 DR Signal: Immunoglobulin domain; Multigene family; Neurogenesis;
 KW development; protein; Glycoprotein.
 KW SIGNAL 1 22
 FT CHAIN 1 23 772
 FT DOMAIN 240 538
 FT DOMAIN 643 730
 FT DOMAIN 728 770
 FT DISULFID 650 723
 FT CARBOHYD 53 53
 FT CARBOHYD 125 125
 FT CARBOHYD 591 591
 SQ SEQUENCE 772 AA; 88867 MW; E91E09DECC940AC CRC64;

Query Match 17.5%; Score 632.5; DB 1; Length 772;

Best Local Similarity 28.4%; Pred. No. 5e-40;
 Matches 195; Conservative 101; Mismatches 265; Indels 125; Gaps 28;

29 LRLRLLLMAAASAOGLRSGPRIFAVMKGVGQDR-VDF---GQTEPHTVLFHEPG 83
 7 IALLSLGVLARANYANGKNNVPRKLSTYKEMLESNNVITFNGLANSSVHTFLDDE- 65
 84 SSVVWVGGRKGYLLDFPEPGKNAVRYVNICSTK-----GSKKSCV-----DKRDE 127
 66 RSRLYVGAKDHIFSFNL-----VNIKEYOKIWPVSVYTRDECKMAGKDIKLRCA 115

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QY 128 NYITTLERSE-GLACGTNARHPSGMNVNGLVPLGEM-----RGTA 170
DB 116 NIKALKYNTNHLACGAGAPMC-----TYLEVGHEDNIFRMDSEFENRGKS 169
QY 171 PPSDENSLVLEEGDEVSTIRKOEYNGKIPRRIRIGSELYT---SDTVQNPQFIKA 227
DB 170 PYDPLRLTASLVDELIVSGTADMGKRFALFRILGHHHPRTEDHDSRWMLNDREFISA 229
QY 228 TIV-HODAYVDKIYFPREDNPKNPEAPLVASRYAOLCRGDGESSLSVSKMNTFLK 286
DB 230 HLPESDENPDEDKIYFFEFENALDEGHTGKATHARIGQCKNDGFGHRL-VNKKWTFELK 288
QY 287 AMLVCSDATN---KNPNRLQVFL--PDPSGQMRDTRVYGVF---SNPMYKSAVCYS 338
DB 289 AKLISVPGPNIDITHFELQVFLMNSKDP---KNPLVYVFTTSSNIFKGSVAVCMS 344
QY 339 LGDIDKVF-----RTSSLKGYSLLPNRPGKC-----LPDQDPIPTETFOVAD 382
DB 345 MTDVARRVFLGPRAHADGPNYQWVPYQGRVYPRPGTCSKTFGDFDSTKDLDEVYTTAR 404
QY 383 RHPEVAQRYEPMGP---LKTPLFHSKYHYQKAVAHMQASHGETPHVLYLTTRGTIHK 438
DB 405 SHPAMYNVFPIINSRPIKTDV---DYQFQIVDVADEGQ-YDVWFIQTDIGTVLK 460
QY 439 VYE-FGEQHSFAFNIM-EIOFPRAAAIQYMSLDAERKLYVSSQWESQVPLDCEY 496
DB 461 VYSIKETWHELEEVLEEMTFEPTVISAARKISTKQOLIGSATGVSQPLHRCDY 520
QY 497 GGGCGHCLMSRDPYCGMDOGRCSISY---SSERSVLOSINPAEPHKEC-----PNPKDPK 548
DB 521 GKACHECLARDPYCAMGSSCSRYFPKAKRTKRODIRNGDPLRHCSDLQHDNDPSCOT 580
QY 549 APLQKVSILAPNSRYLLSCPMESRHAATYSWR-----HKEVNEQS-----CEPGHQPNC 596
DB 581 LEKIKIYGVENSSTFLECSPSQRAIYVQFQKNDHKVEIKVDRIKRTFQG----- 634
QY 597 ILFENLTAQOYGHCECAOEGSYFR 622
DB 635 -LLKSLQDRDSGLYFCHAVEHGTIO 659

RESULT 6
SM3B_MOUSE
ID SM3B_MOUSE STANDARD: PRT: 748 AA.
AC Q62177;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Semaphorin 3B precursor (Semaphorin A) (Sema A).
GN SEMA3B OR SEMA OR SEMA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Embryo;
RX MEDLINE=95267431; PubMed=7748561;
RA Pleschel A.W., Adams R.H., Betz H.;
RT "Murine semaphorin D/collapsin is a member of a diverse gene family
RT and creates domains inhibitory for axonal extension.";
RL Neuron 14:941-948(1995).
CC -1- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SIGNALS TO
CC SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- DEVELOPMENTAL STAGE: EXPRESSED FROM DAY 10 IN THE EMBRYO. LOW
CC LEVELS FOUND BETWEEN DAYS 10-12. EXPRESSION PEAKS ON DAY 13 WITH
CC MODERATE LEVELS FROM THEN UNTIL BIRTH.
CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
CC -1- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
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CC
DB EMBL: X85990; CAA5982.1; -.
DR MGD: MGI:107561; Sema3b.
DR InterPro: IPR003599; 1g.
DR InterPro: IPR003006; 1g.MHC.
DR InterPro: IPR003659; Plexin-like.
DR InterPro: IPR001627; Sema.
DR Pfam: PF00047; 1g.
DR SMART: SM00409; IG.
DR SMART: SM00423; PSI.
KW Signal. Immunoglobulin domain; Multigene family; Neurogenesis;
KW Developmental protein; Glycoprotein.
FT SIGNAL 1 25
FT CHAIN 26 748 SEMAPHORIN 3B.
FT DOMAIN 239 536 SEMA.
FT DOMAIN 636 716 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 698 702 POLY-GLY.
FT DOMAIN 723 743 ARG-RICH (BASIC).
FT DISULF 643 709 BY SIMILARITY.
FT CARBOHD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 748 AA; 82894 MW; 1668BD2397C9305 CnC64;

Query Match 17.4%; Score 628.5; DB 1; Length 748;
Best Local Similarity 31.5%; Pred. No. 9.7e-40;
Matches 181; Conservative 76; Mismatches 244; Indels 73; Gaps 21;

QY 125 DEENTTLERSE-GLACGTNARHPSG---WLVNGLVPLG-----EMRGYAPESP 174
DB 112 ECMANFVRLHAYNTHNLACRTGAFHPICALMKWATAGTASTPEKLEDKGTPIDP 171
QY 175 DENSLVLEEGDEVSTIRKOEYNGKIPRRIRIGSELYT---SDTVQNPQFIKA-71V 230
DB 172 RHRPSVILGEELYSGVATDLKGRDFTIFRSIGQNPISLRTBPHDSRWMLNEPRFVFWNP 231
QY 231 HODAYVDKIYFPREDNPKNPE-APLVASRYAOLCRGDGESSLSVSKMNTFLKML 289
DB 232 ESENDPDKIYFFEFESAVEAAPAMGRMSVSRVQICRNDLGQSL-VNKKWTFELKARL 290
QY 290 VCS---DAATNKNFNRLQVFLPLDPGQWRDT-RVYGVSNP---WNSAVCVSLGIDID 343
DB 291 VCSYVGEVDTHFDQLOVFL---SSRDROTPLLYAVFTSSGVFGQSAYCVISMNDVR 347
QY 344 KVF-----RTSSLKGYSLLPNRPGKC-----LPDQDPIPTETFOVADRHPEV 387
DB 348 RAFLGLPLHKEGPQHWSYQGRVYPRPGMCPSTKTFGFSSTKDFPDVIOFGNHPLM 407
QY 388 AQRVPRPKLTPLE---HSKYHYQKAVAHMQASHGETPHVLYLTTRGTIHKV--YEP 442
DB 408 YNPVLPNG--GRPLFLOVAGAGTFTQIADRAVAADG-YDVLFTGTGVYGLKYISPK 464
QY 443 GEOSFNFNIMEIOPFRRAAIQYMSLDAERKLYVSSQWESQVPLDCEVYGGCGH 502
DB 465 GRPNSGELLLEQVFDSDAITSMTQISSKROULYASRAVAOIALHRTALGRACAE 524
QY 503 CLMSRDPYCGMDOGRCSISY---SSERSVLOSINPAEPHKECPNPKAPLQKVSILAPNS 560
DB 525 CCLARDPYCAMDGSCTFQPTAKRFRQDIRNGDPTLCSGSHSVLLEKLVGES 584
QY 561 RYILSCMESRHAATYSKR-----KENVQCEPQHQSNCILFENLTAQ 606
DB 585 GSAPLECEPRSLQAHVQWTFQAGAAHTQVLAERVERTARG-----LLLRGLRQ 636
QY 607 QYGHVCEAOGSYFREAOHQMLLPEDIGMAEHL 640
DB 637 DSGVILCAVAEQGFSQPLRLVYLHLVLSAQAEHL 670

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SQ SEQUENCE 772 AA: 88808 MW: 240907812FP9F2D2 CNG64: .
 Query Match 17.2%; Score 623; DB 1; Length 772;
 Best Local Similarity 27.7%; Pred. No.2.6e-39;
 Matches 190; Conservative 108; Misses 287; Indels 100; Gaps 26;
 QY LLMMAASAGCHLRG-----PRIFAVMKGHVQDDVD-----FGQTEPHTVLFHRRGSS 86
 DB 10 LFWGILLTARAVYANGKNNVPRKLSTYKEMESNNVITFNGIANSSYHTFLDEE-RSR 68
 QY VVWGRGKYLLEDPFGKNAVRVYNIGSTK-----GSCDKRDKCENYITLLRRSE- 138
 DB 87 VVWGRGKYLLEDPFGKNAVRVYNIGSTK-----GSCDKRDKCENYITLLRRSE- 138
 DB 69 LVGAKDHIFESNLVNIKDFQKIVPVYSTRRDECKMAGKDLK-ECANFIKVLKAYNQ 127
 QY 139 GLLACGTNARHPSCHNLVNGVTVPLGEM-----RGYAFSPDENSELVLF 182
 DB 128 HLYAGCTGAFHPIG-----TYIEVGHNEEDNIFKLODHFENGSGKSPYDEKLLTASLL 181
 QY 183 EEDVEYSTIRKEVNGKIPRRIRIGESELY---SDPYMNPORIKATIV-HOQAADD 238
 DB 182 IDGELYSGTADPFMRDPAIFFTLGHNHPIRQSDSRMLNPRFISHLIPESNPPDD 241
 QY 239 KIYFFREEDNPKNENAPLVNSRVNQLRGDGGESSLSVSKMNFILKAMLVCAATN- 297
 DB 242 KYIFFRENAIDGESHGKATARIQICKNDFGGHRS-LVKNWITTFLLARLICSYPENG 300
 QY 298 --KNFNRLODFLL--PDPSGWRDTRVYGVF--SNPNYSAVCVSLGIDIKVF--- 346
 DB 301 IDTHFDELDDVFLMSKDP---KNPIYGVPTSSNIFKGSAYCMYSMSDVRVFLGPY 356
 QY 347 -----RTSLKKNYHSLPRPRGKC-----LPDQQRPIPTFGVADNRHVEVQARVERPM 394
 DB 357 AHRDGNTOVWPYQGRVPRPRPGTSPKTEGGFSDTKDLPDVIDTFANSHPRAMYVPEPI 416
 QY 395 G----PLKPTFHSKYHOKVAVNHMQASHGTFHVLITLRTGTILHKVE--PGEQSEHF 449
 DB 417 NNRPIMKTDV---NYQFTQIVYDVRVADBDG-YDMFGLGTGVYLVKAVSPKRTWML 472
 QY 450 AFNIM-ETQPFRRAAIQTMSLDAERKRLVSSQMEVSOVPLDLCEVYGGCGHGLMSRD 508
 DB 473 EVELLEEMTVFEEPTTISIMELSTKQOOLYISTAGVQDLPHRDDIYGKACAECCCLARD 532
 QY 509 PRCGMDGQGCISTY---SSRSVLQSLINPAERHKEC-----PNRPDKAPLDQVSLANS 560
 DB 533 PRCAMDGSSCSRYFPAAKRTRRDRIKNGDPLTHCSDLQHNHNGHSLSEERIIIGVENS 592
 QY 561 RYVLCSPMSESRATYSMKRIKENVEDSCPEGHQSPNCI-----LTETNLAQGYAFCEA 615
 DB 593 STFFLECSPRSQALVYVQQRNDRKEIRRGDHIIRTEQGLLRSLQKDSGNVLC 652
 QY 616 QEGSYFREAOHWQLLPEDGIMAEHL 640
 DB 653 VEHGFQTLTKVTL--EVIDTEHL 674
 RESULT 8
 SZ1A_BRARE ID SZ1A_BRARE STANDARD: PRT: 860 AA.
 AC 09W7J1:
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Semaphorin z1a precursor (Semaphorin 1A) (Sema-z1a).
 GN SEMA21A OR SEMA31A.
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxId=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 MEDLINE=99313409; PubMed=10386838;

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RA Yee C.S., Chandrasekhar A., Halloran M.C., Shoji W., Warren J.T.,
RA Kuwada J.Y.;
RT "Molecular cloning, expression, and activity of zebrafish semaphorin
RT zia."
RL Brain Res. Bull. 48:581-593(1999).
CC -1- FUNCTION: MAY INFLUENCE OUTGROWTH BY A VARIETY OF GROWTH CONES
CC INCLUDING THOSE OF THE POSTERIOR LATERAL LINE GANGLION.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN HIGHLY SPECIFIC PATTERNS WITHIN
CC THE DEVELOPING EMBRYO.
CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
CC -1- SIMILARITY: CONTAINS 1 SEMAPHORIN-LIKE C2-TYPE DOMAIN.
CC -----
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CC -----
DB EMBL: AF06761; AAD43964.1; -.
DB XFIN: ZDB-GENE-991209-3; sema3aa.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003659; Plexin-like.
DR InterPro: IPR001627; Sema.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF01403; Sema; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00423; PST; 1.
DR Signal: Immunoglobulin domain; Multigene family; Neurogenesis;
KW Developmental protein; Glycoprotein.
FT SIGNAL 1 17
FT CHAIN 18 860
FT DOMAIN 241 539 SEMAPHORIN 21A.
FT DOMAIN 645 724
FT DOMAIN 722 858
FT DISULFID 652 717
FT CARBOHYD 53 53
FT CARBOHYD 126 126
FT CARBOHYD 593 593 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 860 AA: 97263 MW: 5FDAC12194F5165C CRC64;

Query Match 17.2%; Score 621; DB 1; Length 860;
Best Local Similarity 26.5%; Pred. No. 4.3e-39;
Matches 194; Conservative 107; Mismatches 256; Indels 176; Gaps 31;

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QY 311 DPGQWDRTRVYGVF---SNPMNTSAVCVSLGIDKVFRTSLKGY-HSSLPN----- 360
DB 319 DP-----KNPVIYAVFTTSSNLFRCGSAICMYSMDIRVFE-----LGPYAHRCGPYQWVPE 370
QY 361 -----PRPGK-----LPDQRPPIPTETQVADRHEVAGQREBPMLKTPLE---HS 404
DB 371 QGRVYPRPGHCPSKTEGCFDSTDLDPDVTTFARLHPAMNPQPMG--GKPIVTRTNV 428
QY 405 KYHOKVAVHNMQASHGFTFVLTITDRGTIHYVE--PGEOESHFAPNIN--EIOPFRRA 462
DB 429 EYQFTQLVNDVVEADGQ--YDMFTGIDLTGLVAVTTPRESMHDLEUVLEMTVREPR 487
QY 463 AAIGTMSDAERRLVYSSQWEVSQVPLDCEVYGGCGHCLMSRDPYCGMDGRCISIV 522
DB 488 TPIMAEIETKQOOLYGSGLDISOMPLHRCVEYVGKACAECCCLARDPYCAMDTECSRFE 547
QY 523 ---SSERSVLOSINAEPRIKECPNRPD-----KAPLOKSLAPNSYTYLSCMESRHA 573
DB 548 PTARRRTRRQDIRNGDPLQCSDLHHNDDEGYSSVEERSVYGVNSSFLECSPRKSQRA 607
QY 574 TYSW-----RRKEVQSCPEGHQSPNCILFIEMLTAQYGHYCFEAGQESYFREA 624
DB 608 LIYQLOKPNRDKHEIYIDERSLTGG-----LLIRSLTADSGVFLCHAVENGFIQPL 663
QY 625 Q--HWQLPEDGI 635
DB 664 RRLNQLVIPSQV 676

RESULT 9
SM3B_HUMAN STANDARD; PRT; 749 AA.
ID SM3B_HUMAN
AC Q13214; Q93018;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Semaphorin 3B precursor (Semaphorin V) (Sema V).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96210603; PubMed=8633026;
RA Sekido Y., Bader S., Latif F., Chen J.-Y., Duh F.-M., Wei M.-H.,
RA Albanesi J.P., Lee C.-C., Lerman M.I., Mina J.D.;
RT "Human semaphorin A(V) and IV reside in the 3p21.3 small cell lung
RT cancer deletion region and demonstrate distinct expression patterns."
RT Proc. Natl. Acad. Sci. U.S.A. 93:4120-4125(1996).
RL [2]
RP SEQUENCE FROM N.A.
RA Dante M., Mamsley P.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SIGNALS TO
CC SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY). ACCUMULATES IN THE
CC ENDOPLASMIC RETICULUM.
CC -1- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY BUT DIFFERENTIALLY IN A
CC VARIETY OF NEURAL AND NONNEURAL TISSUES.
CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
CC -1- SIMILARITY: CONTAINS 1 SEMAPHORIN-LIKE C2-TYPE DOMAIN.
CC -----
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FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 526 526 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 574 574 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 639 639 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 782 AA; 86823 MW; 627A81FC8F87AC8 CRC64;

Query Match 17.1%; Score 617; DB 1; Length 782;
Best Local Similarity 30.4%; Pred. No. 7.6e-39;
Matches 193; Conservative 91; Mismatches 253; Indels 98; Gaps 28;

QY 75 HTVLFGHGGSSVWVGGRKYYLFD----FPEKMASVTRVNIIGTKSGCL----DKR 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 16 YTALLLSQDCKTLVYGAREALFALNSNLSPFJGGEYDELLMSADADRKQCSFKGDKPKR 75

QY 125 DCEYVI-TLLERSEGLACGTNAHPSC-----NWLNV---GTVPLDEMGYAFS 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 76 DCQYVITILLPLNSSLHLLTCTAASPICAYITHASFTLADDEAGNVI-LEDGKGHCPED 134

QY 174 PDENSLVFEGDEVYSTIRKQEVNGKIPREFRIGESELELYSDTV--WQNPQFIKATIVH 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 135 PNEKSTALVVDGELY-IGTVSSFOGNDPAISRSQSSRPTKTESLNLMDQDAFAVASATSP 193

QY 232 QDAAY----DGIYFFREDNPDKNPEAPLVNRYAOLCRDQGGESLSVSKNNTFLKA 287
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 194 ESLSPIGDDDKIYFFSEFGQEEFEFENTIVSRVARCKDEGGERVLO-QRWTSFLKA 252

QY 288 MLVCSDATNKNFNRLDDVFL-PPDSGQWRDTRVYGFNSPMNV-----SAYCVYSLGD 341
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 253 QILCSRDDGPFENVLDVFTLNPNPO-DWRKTLISIGFTSQMHRGTGSAICVFTIAND 311

QY 342 IDKYF-----RTSSLGKHYSSLNPRGKCLPD--QQPIETFTVADR----- 383
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 312 VQKAFDCLYKKVNETQWYETHTQVPTPRACITNSAREKINSSQLDRLVNLFLKD 371

QY 384 ----HPEVAQVERPMGLKPTPLFSKXHYQKVAVHRMAGSGEFHYHLTDDGTITIKV 439
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 372 HFLMDGVRSLRLLLP-----RAKYQVAVHRVPGHL-STYVDVLTGTDGRLHKA 422

QY 440 VEPGEQSHFANIMEIOTPFRRAAIOTMSDARRKLYVSSQMEVSOPVLDCEVGGG 499
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 423 VTLSSRHH-----TELODFPGOPVONLLDHSGLLYASHSGVQVVPANCSLY-PT 477

QY 500 CHGCLMSRDYCGMDGRC--ISIVS--SERVYLQSLNPAEPHKECPNPK-----PD 547
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 478 CGDGLARDPYCAWGTGSACRLASLYQPLDASRPWTODIEGASVKELCNKSYSKARFLVPG 537

QY 548 KAPLOKYSIAPNSRYLISCPRESRHATYSWRHKEVNEOSCEPQGSPRC-ILFTENL--- 603
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 538 K-PEKVOIOPNTVNTLACPLSLMLATRLVNH-----NGAPVNASASCRVLPDGLLLV 590

QY 604 -TAQOYGHYFC-EAOGSSYFREAOHMOILLPEDGIM 636
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 591 GSQOGLGVFOCMSTIEBGFQOLVASYCEPVMEGVM 625

RESULT 11
SZ1B_BRARE
ID SZ1B_BRARE STANDARD; PRT; 778 AA.
AC 09M686;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Semaphorin 21B precursor (Semaphorin 1B) (Sema-21B).
GN SEMA21B OR SEMA3AB
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RA MEDLINE=99425174; PubMed=10495275;
RX Roos M., Schacher M., Bernhardt R.R.;
RT "zebrafish semaphorin 21b inhibits growing motor axons in vivo.";
RL Mech. Dev. 87:103-117(1999).
CC -1- FUNCTION: MIGHT NORMALLY INFLUENCE THE MIDSEGMENTAL PATHWAY CHOICE
CC OF THE VENTRALLY EXTENDING MOTOR AXONS BY CONTRIBUTING TO A
CC REPULSIVE DOMAIN IN THE POSTERIOR SOMITE.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN RHOMBOMERES THREE AND FIVE, AND
CC IN THE POSTERIOR HALF OF NEWLY FORMED SOMITES WHICH IS AVOIDED BY
CC VENTRALLY EXTENDING MOTOR AXONS.
CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL, AF083382; AAD28103.1; -
DR ZFIN; ZDB-GENE-991209-6; sema3ab.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003659; plexin-like.
DR InterPro; IPR002165; plexin_repeat.
DR InterPro; IPR001627; Sema.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF01403; Sema; 1.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00423; PSI; 1.
KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
KW Developmental protein; Glycoprotein.
FT SIGNAL 1..17
FT CHAIN 18..778
FT DOMAIN 241..539
FT DOMAIN 645..723
FT DOMAIN 721..776
FT DISULFID 652..716
FT CARBOHYD 54 34
FT CARBOHYD 127 127
FT CARBOHYD 593 593
SQ SEQUENCE 778 AA; 88904 MW; 4D36F4323AE21895 CRC64;

Query Match 17.0%; Score 613; DB 1; Length 778;
Best Local Similarity 29.0%; Pred. No. 1.3e-38;
Matches 204; Conservative 111; Mismatches 260; Indels 128; Gaps 36;

QY 33 LLLLLMAAASAOCHL-----RSGPRIFAVWKGVH-GQDRVDF-----GQTEPHVLFHEP 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 7 IVLLIWTLLIAFERGTVAQRKSNVPRKPSYKEMLESNLLTFNGLANSSAYHFFLLDEE 66

QY 83 GSSSVWVGGRGKYYLFDPEEGKNASVTRVNI-----STKGSL-----DKRDC 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 67 -RGRLEFGAKDHVLSFNLVD-----INMDQLISWSSPSRDECKWAKGVOKRECA 117

QY 128 NYITLLERRSE-GLLACGTNAHPSCNMLVNG-----TVPLGEM-----KTAAPSPD-E 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 118 NFIVVLQPFNFQTHLYACGTGAFHVCAGHVEGKRSSEDTFRIGSSFENGKRSYDRLQ 177

QY 177 NSVLFGDEVYSTIRKQEVNGKIPREFRIGESELYT---SDTVMNQPIKATIV-HQ 232
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 178 TASMLDGE-ELYAGTSADENMGKDPFAIRFTTGLKHHPIRTEQDHSWLDNPRFVSHLIPES 236

QY 233 DOAEDDKIYFFREDNPDKNPEAPLVNRYAOLCRDQGGESLSVSKNNTFLKAMLVCS 292
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 237 DNAEDDKIYFFRENAIDGDISKATHARIGQLCKNDFGGRSL-VKMTTFFLARLVCS 295

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0Y 223 DAATN- ---KXNRLNODVYLL- -PERSQOMRTBYGVF- ---SNMWNANSVCVYSLGIDK 344
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 236 VPGMGIDTHTDELDODVFLMKSQR- ---KXPIIYAVFTTSSNIFKGSAYCMM5MAAIR 351
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
0Y 345 VERTSLSLKG- -HSSLPN- ---PRGKC- ---LFDQOPITETFOVADRI 384
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 352 VF- ---LGRYAHROGSRNQQWPRPLNRYRYPYRPGCRPKETDGFESTKDFDDVITFARSH 407
      ::::: ::::: ::::: ::::: ::::: ::::: :::::
0Y 385 PEVAORVERMGR- ---LKTPLNHSKYNIOKAVNRMQASNGEFPNVLUTPTDKTINKV 440
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 408 PAMYRVPYRINNHPRIITKTDV- ---DYOFOTQIVUDRYVAEADGQ- -YDVAFISTDMGTVLKV 463
      ::::: ::::: ::::: ::::: ::::: ::::: :::::
0Y 441 E-PGRGHSFANIM-ELQPRRRAAATQTM5LDBERRKLVSSQWME5QVURLDCEVGG 468
      ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 464 SIPRGTHTDLEEVLLLEEMTVREPTATAMELSTKQOOLIGSIAIG5QMPILNRCDYGG 523
      ::::: ::::: ::::: ::::: ::::: ::::: :::::
      499 GCHGCLMSRDEYCGMDGRCISY- -SSESRVLQ5INPAERHKECPN-PRDKAP 550
      ::::: ::::: ::::: ::::: ::::: ::::: :::::
      524 ACAECCLLARDYCAMDGSQCSRYPTAKRRIRRDINDGRPLTQCSLDQNDHDEADGAGL 563
      ::::: ::::: ::::: ::::: ::::: :::::
0Y 551 LQK- -V5LAPNSRYVLSCPMESRHAITYSR- ---HKEYNEQ- ---SCERGHQSPNCI 597
      ::::: ::::: ::::: ::::: ::::: :::::
Db 584 LDKTYGVGENSSSFLECSPKQORALITYOFORHGEDHKLKIKSDERVLTGETOG- --- 636
      ::::: ::::: ::::: ::::: :::::
0Y 598 LFIENTLAAOYGHYPCSEAOES5YRRAOHWOLDPEQDITMAEHL 640
      ::::: ::::: ::::: ::::: :::::
Db 637 LLIRSLHOKD5GVYCAVAENGFIQTLLRLTL- ---NIPIAEHL 676
      ::::: ::::: ::::: :::::

```

DR	InterPro: IPR003659; Plexin-like	
DR	InterPro: IPR002165; plexin_repeat.	
DR	InterPro: IPR001627; Sema.	
DR	Pfam: PF00047; Ig; 1.	
DR	Pfam: PF01403; Sema; 1.	
DR	Pfam: PF01437; PSI; 1.	
DR	SMART: SM00408; TGC2; 1.	
DR	SMART: SM00423; PSI; 1.	
KW	Signal; Transmembrane; Immunoglobulin domain; Multigene family; Neutrogenesis; Developmental protein; Glycoprotein.	
FT	SIGNAL	1 23
FT	CHAIN	24 861
FT	DOMAIN	24 733
FT	TRANSMEM	734 754
FT	DOMAIN	755 861
FT	DOMAIN	228 523
FT	DOMAIN	569 630
FT	DISULFID	576 624
FT	CARBOHYD	49 49
FT	CARBOHYD	77 77
FT	CARBOHYD	139 139
FT	CARBOHYD	191 191
FT	CARBOHYD	379 379
FT	CARBOHYD	419 419
FT	CARBOHYD	613 613
FT	CARBOHYD	632 632
SEQ	SEQUENCE	861 AA: 95714 MW: 533060

RESULT 12	SM4D_MOUSE	STANDARD:	PRT:	861 AA.
DR	SM4D_MOUSE			
AC	009126;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Semaphorin 4D precursor (Semaphorin J) (Sema J) (Semaphorin C-like 2) (M-Sema G).			
CN	SEMA4D OR SEMAJ OR SEMACL2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
	SEQUENCE FROM N.A.			
	STRAIN=C57BL/6; TISSUE=Brain;			
	MEDLINE=97125976; PubMed=8969198;			
RA	Furuyama T., Inagaki S., Kosugi A., Noda S., Saitoh S.-I., Ogata M.,			
RA	Iwatsubashi Y., Miyazaki N., Hamooka T., Tohyama M.;			
RT	"Identification of a novel transmembrane semaphorin expressed on			
RT	lymphocytes.";			
RL	J. Biol. Chem. 271:33376-33381(1996).			
CC	- FUNCTION: MAY PLAY A FUNCTIONAL ROLE IN THE IMMUNE SYSTEM, AS WELL			
CC	AS IN THE NERVOUS SYSTEM.			
CC	- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN LYMPHOID TISSUES,			
CC	ESPECIALLY IN THE THYMUS, AS WELL AS IN THE NERVOUS TISSUES.			
CC	- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.			
CC	- SIMILARITY: CONTAINS 1 SEMA DOMAIN.			
CC	- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: U69535; AAC52964.1; -			
DR	MGD: MGI:109244; Sema4d.			
DR	InterPro: IPR003006; I9_MHC.			
DR	InterPro: IPR003598; I9_C2.			

[illegible]

DB 550 TSSCLDKSNEHNFHFKGTAELKCFOKSNLARVWKFQNGELKASPKGVGRKH- 608

QY 595 NCILEFENLTAAQYGHFCEAGGSGYFREAQHMOLLPEDEGIAEHL 641

DB 609 ---LTIENLSDGSDGYCQLSEE--RVRNKTVSOLL-----AKHYL 644

RESULT 13

SM3C_MOUSE STANDARD: PRT: 751 AA.

AC 062181;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Semaphorin 3C precursor (Semaphorin E) (Sema E).

GN SEMA3C OR SEMAE OR SEME.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RE SEQUENCE FROM N.A.

RA STRAIN=NMRI; TISSUE=Embryo;

RA MEDLINE=95267431; PubMed=7748561;

RA Puschel A.W., Adams R.H., Betz H.;

RT "Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.";

RL Neuron 14:941-948(1995).

CC -1- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SIGNALS TO SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS.

CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -1- DEVELOPMENTAL STAGE: EXPRESSED FROM DAY 10 IN THE EMBRYO. MAXIMUM EXPRESSION BETWEEN DAYS 10-12 WITH MODERATE LEVELS FROM DAY 13 UNTIL BIRTH.

CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.

CC -1- SIMILARITY: CONTAINS 1 SEMA DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

CC -----

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CC -----

DR EMBL; X85994; CA59986.1; ..

DR MGD; MGI:107557; Sema3c.

DR InterPro: IPR003599; Ig.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003659; plexin-like.

DR InterPro: IPR001627; Sema.

DR Pfam; PF00047; Ig. 1.

DR SMART; SM00409; IG. 1.

DR SMART; SM00423; PST. 1.

KM Signal: Immunoglobulin domain; Multigene family; Neurogenesis;

KM Developmental protein; Glycoprotein.

FT SIGNAL 1 20

FT CHAIN 21 751

FT DOMAIN 237 535

FT DOMAIN 636 716

FT DOMAIN 714 717

FT DOMAIN 724 745

FT DISULFID 643 709

FT CARBOHYD 81 81

FT CARBOHYD 123 123

FT CARBOHYD 252 252

FT CARBOHYD 268 268

FT CARBOHYD 465 465

FT CARBOHYD 585 585

FT CARBOHYD 586 586

N-TERMINAL. POTENTIAL.

SEMAPHORIN 3C.

IG-LIKE C2-TYPE DOMAIN.

POLY-GLN.

ARG/LYS-RICH (BASIC).

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQ SEQUENCE 751 AA: 85259 MW: A9B599E5E7DB45D8 CRC64:

Query Match 16.5%; Score 597.5; DB 1; Length 751;

Best Local Similarity 28.8%; Pred. No. 2,1e-37;

Matches 175; Conservative 96; Mismatches 265; Indels 71; Gaps 23;

QY 75 HTVLFHEPGSSVWVGKGVYLFDFPECKNAS-----VFVINGSTGSCID-KR 124

DB 54 YKLLMDEDDQDRIVYOSKDHILSLNI---NNISOEPLSVFMPASTIKVECKMAGKDP 110

QY 125 DCENYITLLER-RSEGLACGTFNARHPSGWNLVNG-----TVPLGEM-----RGARFSP 174

DB 111 GCGNFRVYIQTNRNHLIYCGGAFSPVCTYLNKGRSDQYFMIDSKCESSGRCGSP 170

QY 175 DENSLVLEEGDEVSTIRKQEVNGKIPRRRIKGESELYT---SDPTMKNPOFIKATIVH 231

DB 171 NVNTVSMINEBELFGMYIDFGTDAIIPRLITKRMLQTLDDGNSKWLSEPFVDAHV 230

QY 232 Q-DQAVDDKIYFFREDNDKRPAPLVNRYAOLCRGOGGESSLSVSKMTFLKAMLY 290

DB 231 DGTDPNDAKVYFFERLTDNNRSTKQIHSMIARICPDNTGGQRL-VKMTTFPKARLV 289

QY 291 CS---DAATNKNFNLQVFLLPDPSGQWRDTRVYGVF---SNPNVSAVCYSLGIDDK 344

DB 290 CSVTDEDEGETHFDLEEDVFLLETDPNP--RTLLVYGIFTTSSSVKGSVAVCYHLSDIOT 347

QY 345 VFR-----TSLKGYHSSLPNRPDKC-----LPDQDPIPTETFGVADRHPEV 387

DB 348 VENGPFARKEGPHNOLISVQGRIPYRPRTCPGCAFTPRMTTKDFPDVVYFIRNPLM 407

QY 388 AGRVPMPLKPLPL---FHSKHYOKVAVNRQASHGEFHNLYLTTRGTGTHKVE-PG 443

DB 408 YNSISPIH--RRPLLVRIGTDKYRKIVADRVNADGR-YHVLFGTRGVQKVVVLEPT 464

QY 444 EDEHSAFNIMEIOPEFRRAAIOTMSLDAERKELVSSQWESQVPLDCEVYGGGCHG 503

DB 465 NSSAGGELLELEVFKNHVPITTMIEISKQOLYVSSNEGVSQVSLRCHITGTACADC 524

QY 504 LMSRDPYCGMDGRCISLY--SSERSVLQSNIPAPRKECP--NPKPKAPLQKYSL-AP 558

DB 525 CLARPYCAMGHSCSRFYPGKRRSRQDVRHGNDPLQCRGFNLKAVRNAAEIYQVCR 584

QY 559 NSRYLSCPMSRHATYMRKHEVQSCPCGHOSPNCI-----FLENLTAAQYGHFEC 613

DB 565 NNSFTLECAPKSPQASIKWLQDKDRKE-GKLERIATISQGLLIRSVODSDGLVHC 643

QY 614 EAQEGSY 620

DB 644 IATENSEF 650

RESULT 14

SM3F_HUMAN STANDARD: PRT: 785 AA.

ID SM3F_HUMAN Q13275; Q13274;

AC Q13275; Q13274; Q13274; Q13274;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Semaphorin 3F precursor (Semaphorin IV) (Sema IV) (Sema III/F).

GN SEMA3F.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RE SEQUENCE FROM N.A.

RA TISSUE=Fetal brain;

RA MEDLINE=96226360; PubMed=8649831;

RA Roche J., Boldo F., Robinson M., Robinson L., Varela-Garcia M., Swanton M., Waggoner B., Fishel R., Franklin W., Gemmill R., Drabkin H.;

RT "Distinct 3p21.3 deletions in lung cancer and identification of a new human semaphorin.";

FT	CONFLICT	270	270	MISSING (IN REF. 2).
FT	CONFLICT	473	473	A -> S (IN REF. 2).
SQ	SEQUENCE	785 AA;	88381 MM;	FE3FC796EEC1608E CRC64;
Query Match		16.5%;	Score 597;	DB 1; Length 785;
Best Local Similarity		26.0%;	Pred. No. 2.5e-37;	
Matches 194;		Conservative 116;	Mismatches 279;	Indels 156; Gaps 32;
QY	35	LLMAAAS-----AGHLRSGRIFAVAKGHVGDQVDVFG---QTEPTVLFEHPG	83	
Db	6	LLMAALTYGAMPSPHPTODHLPATPRVRLSEKELKATGAHFNFNLMTOTVRLIKDED	65	
QY	84	SSSWVVGGRGVLYLDFDEEGKN-----ASVRVYNIGSRKSGSLDRDCEYITLLE-	134	
Db	66	HDRLMVGSKDYVLSLDLHDINREPLLIHMAASPORIECVLSGKDVN--GEGCNEVRLIOP	124	
QY	135	-RRSGELACGTNARHPSC-----W-----NLVNGTVVP-----	162	
Db	125	WNRTH-LIVCGTGAIVNPCTGVYNGRGAORATPMTQVAVRGSRATGALRPMTAPRQ	183	
QY	163	-----LGMKRGVAFPSPDENSLVLEGEDEVYSTIRKQETNGKIPRRRIIGSESL	212	
Db	184	DYIFLEPERLESGGCKRPDPKLDLTASALINEELVAVYIDFMGTDAIRFTLTKQTAM	243	
QY	213	YT-----SDVPMOPQIFKATIVHO--QAADDKIYFREFDNDPKNEAPLANSVAQLRG	268	
Db	244	RTDQYNSWMLDPSTRIHALLPDSERNDDKILYFFRRRSMAE--PQSAVAVARIQICLN	302	
QY	269	DQGEBSLSVSKWMTFLKAMLYCS---DAATKNFNRLQVDYLLPDPGQWRDTR---VY	322	
Db	303	DDGGHCCL-VAKMSFELKARLVGSPGDDGJETHDELQDVFV-----QQTQDQVNPVIY	356	
QY	323	GVFSNP--WMYSAVCVSLGIDIKVFR-----TSLKGYHSSLPNRPFGKC----	366	
Db	357	AVFTSSGVSFGSAVCYSMDIRKVENGRPAHKKEGPNYQWMPFGKMPYPRPGTCPGCT	416	
QY	367	----LPDQPIPTETFOYADRRPEVAQRVEPMGRPLKPLF---HSKYHVKQVAVHMQAS	419	
Db	417	FTPSKSTKDYPRDEYINFMRSRPLMYQAVYPL--QRRLVYRTGAPVRLTTIAYDVDA	474	
QY	420	HGEFHHVLYLTDDGSTITIKV--VERGEDSHSAFNIMELQPRRAAIIOTMSLDAERKLY	478	
Db	475	DGR-YEVLELTQDTRQVQKVLVLPRLDDELEMLIEEYVKRDPAPVMTTISSRQOOLY	533	
QY	479	VSSOMEVSQVYLDLCEVYGGGCHGCLMSRDYVCGMDQRCISIY---SSESVALOSINPA	535	
Db	534	VASAVGYTHLSLHNGQAAGACADOCCLARDYLCAMD--GQACSRTYASSKRRSRQDVHNG	592	
QY	536	EPHKBCP--NPKRDKAPLQKYSL-APNSRYLLSCPMESRHATYSV-----RHKF--	581	
Db	593	NPIRQCRGFNSNANKNAVESVOYAGVSAALFECQRPSPQATVVKLFFORDGDRRREIRA	652	
QY	582	-----NVQSGCEPGHOSPCILFENTLTAQOYGHFCAQSGSYFREAQHOLLPLPEDI	636	
Db	653	EDRLRFTQGS-----LLRLALDLSRGLYSCATENNNRKHVYTRVOL-----	694	
QY	637	AEHLIGHACALASLWGLVPLTTL	661	
Db	695	-----HVLGRDAVHAA-----LFPPLSM	712	
RESULT 15				
SM22_BRAKE	ID	SM22_BRAKE	STANDARD;	PRT; 764 AA.
AC	Q9W6G6;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Semaphorin 22 precursor (Semaphorin 2) (Sema-22).			
OS	SEMA22 OR SEMA2.			
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			

CC Cyprinidae: Danio.
 OX NCB1_Taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99112778; PubMed-9915572;
 RA Halloran M.C., Severance S.M., Yee C.S., Gemza D.L., Raper J.A.,
 RA "Analysis of a zebrafish semaphorin reveals potential functions in
 RT vivo."
 RT Dev. Dyn. 214:13-25(1999).
 CC - FUNCTION: MAY PLAY A ROLE IN THE GUIDANCE OF SEVERAL AXON
 CC PATHWAYS.
 CC - SUBCELLULAR LOCATION: Secreted (By similarity).
 CC - DEVELOPMENTAL STAGE: EXPRESSED IN A DYNAMIC AND RESTRICTED PATTERN
 CC DURING THE PERIOD OF AXON OUTGROWTH.
 CC - SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
 CC - SIMILARITY: CONTAINS 1 SEMA DOMAIN.
 CC - SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF124485; AAD21310.1; -
 DR ZFIN: ZDB-GENE-990715-2; semaz2.
 DR InterPro: IPR003659; Plexin-like.
 DR InterPro: IPR001627; Sema.
 DR Pfam: PF01403; Sema; 1.
 DR SMART: SM00423; PSI; 1.
 KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT SIGNAL 1 41
 FT CHAIN 42 764 SEMAPHORIN 22.
 FT DOMAIN 261 559 SEMA.
 FT DOMAIN 661 740 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 741 762 ARG/LYS-RICH (BASIC).
 FT DISULFID 668 733 BY SIMILARITY.
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 480 490 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 764 AA; 87859 MW; A3BD95C2479D7AE CRC64;
 Query Match 16.5%; Score 595.5; DB 1; Length 764;
 Best Local Similarity 29.7%; Pred. No. 3, le-37;
 Matches 187; Conservative 105; Mismatches 241; Indels 97; Gaps 30;
 QY 76 TVLFHPGSSVWVGGRGVYLFEPPEGKNAVRYVNIIGSTKG--SCL-----DKRCE 127
 76 TVLDEE--RSRLLGAKDHVYLLD--PDNINKHPKLSMPASRDVEMCILAKGNPLTECA 133
 QY 128 NYITLLERSE--GLACGNNARHPSG-----WNLVNGTVPLPGEMRGVAPESP 174
 134 NPIRVLHSTNRTNHYVACGAGHPPTCALEIKGKEDRWMLLHSTNMGSRMK--CPDP 191
 QY 175 DENSLVLEFGDEVYSPTRKQYNGKIPRRIRNG--ESELV-----TSDTVMKNQFIKA 227
 192 NQPFASVLTQYLYAG--TASDFLGKSTFTRSLSGPPHOQYIRTDISEDYWINEGKFISA 250
 DB 228 TIVHODQAY--DDKIYFFREDNDPKNEAPLNVSRVALQCGDGGSSLSVSKWTF 284
 251 HPI--SDTYNPDODKITYFFREASRDGSTDKSVLSRVARICNDVGLRSLLT--NKWTF 307
 QY 285 LKAMLYCS---DAATNKNRNLQDVFLPDPGQMRDTRVYGF---SNPWNISAVCVYS 338
 308 LKARLYCSIPGPDGYDTHELDIDIFL--PSRDEKNPMVYGVFTTSSIFKGSACVYVT 365
 QY 339 LGDIDKVF--TSSLKG-----YHSSLNPNRPGKC-----LPDQPIPTETFFQVA 381
 DB 366 MEDIRAEFNGPYAHKEGPDHREVEGRILPYRPGTCPSRTYDPHIKTKKDPDEVISPI 425

QY 382 DRHPEVAQRVEPMGRLTKPLF---HSKYHYOKAVAHBMQASHGETFHVLYLTDRGTHK 438
 426 RLHPLAMQSVHPM--TGRPLFTFRINTEYRLQITVDVAADGQ--YAVMLGTDMSGVLK 482
 QY 439 VBERGEQSHFAFNIM-EIOPFRRAAAIQTMSLDAERRLKYSSQWEVSQVPLDCEVYG 497
 483 VSIQENMSSEELIEELQVFNKPSPILMWEVSSKQQLFVGSGDGLVOVSLHRCQIYG 542
 QY 498 GGCHGCLMSRDPYCGMDQGCISTY---SSERSVLOSINAEHPKECPNPKP--DKAPLQ 552
 543 QGCAECCCLARDPYCAMDGTQC--SRVTPASKRRARRQDIKHGDPSSHCWDETVLGRVVE 601
 QY 553 KVLAPNSR--YVLSCPMESRHATYSW-----RHKENVQS-----CEPGHOSPNCILF 599
 DB 602 KVLGYVESNSFLECYSKSQQALIRWFLVLPKGVDRHREINPDERVLTIDRG-----LL 654
 QY 600 IENULTAQVGHYFCEAOEGSYFREAOHWOL 629
 DB 655 IRWLQRGDAGSYFCTSQEHRTFTLLHVS 684

Search completed: March 14, 2003, 09:25:54
 Job time: 14.3094 secs